SEQUENCE LISTING

<110> University of Utah Research Foundation
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<120> VARIANTS OF ANTITHROMBIN III

<130> 21101.0021P1

<150> 60/384,599
<151> 2002-05-31

<160> 93

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Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
            20   25   30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35   40   45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
    50   55   60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65   70   75   80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
                85   90   95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100   105   110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
        115   120   125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
    130   135   140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145   150   155   160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                165   170   175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
Page 14

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                  180                     185                     190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
          195                     200                     205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
      210                     215                     220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                     230                     235                     240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
              245                     250                     255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
          260                     265                     270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
          275                     280                     285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
      290                     295                     300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val His Met Pro Arg
305                     310                     315                     320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
              325                     330                     335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
              340                     345                     350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
          355                     360                     365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
      370                     375                     380
Ala Leu Glu Ala Asn Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                     390                     395                     400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
              405                     410                     415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
          420                     425                     430
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<210> 72
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<210> 73
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<400> 73
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<210> 74
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<400> 76
ctatcgaaaa gccaacaaag cctccaagtt agtatcagc   39

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1   5   10   15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
            20   25   30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35   40   45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
    50   55   60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65   70   75   80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr

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Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
                100               105               110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
            115               120               125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
        130               135               140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145               150               155               160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                165               170               175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180               185               190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
            195               200               205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
210               215               220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225               230               235               240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245               250               255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260               265               270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
            275               280               285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
            290               295               300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305               310               315               320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325               330               335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340               345               350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
            355               360               365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
    370               375               380
Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385               390               395               400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
            405               410               415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420               425               430
```

```
Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1               5                 10                15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
            20                25                30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35                40                45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
    50                55                60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
```

```
65                      70                      75                      80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
                85                      90                      95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100                     105                     110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
            115                     120                     125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
        130                     135                     140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                     150                     155                     160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                165                     170                     175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180                     185                     190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
            195                     200                     205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
    210                     215                     220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                     230                     235                     240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                     250                     255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260                     265                     270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
            275                     280                     285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
        290                     295                     300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                     310                     315                     320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                     330                     335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340                     345                     350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355                     360                     365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
        370                     375                     380
Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                     390                     395                     400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                     410                     415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                     425                     430
```

<210> 79
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 79
```
agccctgtgg acatctgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt        60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag       120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc       180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt       240
atctccacgg ctttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg       300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc       360
tttgccaaac tgaactgccg actctatcga aaagccaaca agcctccaa gttagtatca        420
```
                                Page 18

```
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt        480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc        540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt        600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag        660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct        720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc        780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc        840
ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact cacccccagag       900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc        960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat       1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc       1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg       1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc       1200
aaggccaaca ggcctttcct ggttttttata agagaagttc ctctgaacac tattatcttc      1260
atgggcagag tagccaaccc ttgtgttaag taa                                     1293
```

<210> 80
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 80
```
agtcccgtag atatatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt         60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag        120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc        180
tatcagcacc tggcagattc caagaatgac aatgataaca tttttcctgtc acccctgagt       240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg        300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc        360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca        420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt        480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc        540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt        600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag        660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct        720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc        780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc        840
ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact cacccccagag       900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc        960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat       1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc       1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg       1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc       1200
aaggccaaca ggcctttcct ggttttttata agagaagttc ctctgaacac tattatcttc      1260
atgggcagag tagccaaccc ttgtgttaag taa                                     1293
```

<210> 81
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 81
```
Ser Pro Val Asp Val Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1               5                   10                  15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
                20                  25                  30
```

```
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
    35                  40              45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
    50                  55              60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65                  70              75              80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
                85              90              95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100             105             110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
        115             120             125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
    130             135             140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145             150             155             160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
            165             170             175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180             185             190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
        195             200             205

Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
    210             215             220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225             230             235             240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
            245             250             255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260             265             270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
        275             280             285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
    290             295             300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val His Met Pro Arg
305             310             315             320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
            325             330             335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340             345             350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355             360             365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
    370             375             380
Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385             390             395             400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
            405             410             415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420             425             430
```

<210> 82
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
    synthetic construct

<400> 82
agccctgtgg acgtatgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt   60

```
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag    120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc    180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt    240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg    300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc    360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca    420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt    480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc    540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt    600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag    660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct    720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc    780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc    840
ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact caccccagag    900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc    960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat   1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc   1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg   1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc   1200
aaggccaaca ggcctttcct ggttttttata agagaagttc ctctgaacac tattatcttc   1260
atgggcagag tagccaaccc ttgtgttaag taa                                 1293
```

```
<210> 83
<211> 1293
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 83
agtcccgtag atgtgtgcac agccaagccg cgggacattc ccatgaatcc catgtgcatt     60
taccgctccc cggagaagaa ggcaactgag gatgagggct cagaacagaa gatcccggag    120
gccaccaacc ggcgtgtctg ggaactgtcc aaggccaatt cccgctttgc taccactttc    180
tatcagcacc tggcagattc caagaatgac aatgataaca ttttcctgtc acccctgagt    240
atctccacgg cttttgctat gaccaagctg ggtgcctgta atgacaccct ccagcaactg    300
atggaggtat ttaagtttga caccatatct gagaaaacat ctgatcagat ccacttcttc    360
tttgccaaac tgaactgccg actctatcga aaagccaaca aagcctccaa gttagtatca    420
gccaatcgcc tttttggaga caaatccctt accttcaatg agacctacca ggacatcagt    480
gagttggtat atggagccaa gctccagccc ctggacttca aggaaaatgc agagcaatcc    540
agagcggcca tcaacaaatg ggtgtccaat aagaccgaag gccgaatcac cgatgtcatt    600
ccctcggaag ccatcaatga gctcactgtt ctggtgctgg ttaacaccat ttacttcaag    660
ggcctgtgga agtcaaagtt cagccctgag aacacaagga aggaactgtt ctacaaggct    720
gatggagagt cgtgttcagc atctatgatg taccaggaag gcaagttccg ttatcggcgc    780
gtggctgaag gcacccaggt gcttgagttg cccttcaaag gtgatgacat caccatggtc    840
ctcatcttgc ccaagcctga gaagagcctg gccaaggtgg agaaggaact caccccagag    900
gtgctgcagg agtggctgga tgaattggag gagatgatgc tggtggtcca catgccccgc    960
ttccgcattg aggacggctt cagtttgaag gagcagctgc aagacatggg ccttgtcgat   1020
ctgttcagcc ctgaaaagtc caaactccca ggtattgttg cagaaggccg agatgacctc   1080
tatgtctcag atgcattcca taaggcattt cttgaggtaa atgaagaagg cagtgaagcg   1140
gccgcaagta ccgctctaga ggctcagggc cgttcgctaa accccaacag ggtgactttc   1200
aaggccaaca ggcctttcct ggttttttata agagaagttc ctctgaacac tattatcttc   1260
atgggcagag tagccaaccc ttgtgttaag taa                                 1293
```

```
<210> 84
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct
```

<400> 84
```
Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1               5                   10              15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
            20                  25                  30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35                  40                  45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
        50                  55                  60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65                  70                  75                  80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
                85                  90                  95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100                 105                 110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
        115                 120                 125

Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
        130                 135                 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                 150                 155                 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                165                 170                 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180                 185                 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
        195                 200                 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
        210                 215                 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                 230                 235                 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                 250                 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260                 265                 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
            275                 280                 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
        290                 295                 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                 310                 315                 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                 330                 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340                 345                 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355                 360                 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
        370                 375                 380
Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                 390                 395                 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                405                 410                 415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430
```

<210> 85
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
    synthetic construct

<400> 85
His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
1   5   10   15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
            20   25   30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35   40   45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
    50   55   60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65   70   75   80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                85   90   95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100   105   110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115   120   125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130   135   140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145   150   155   160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
            165   170   175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180   185   190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195   200   205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
    210   215   220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225   230   235   240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
            245   250   255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260   265   270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275   280   285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290   295   300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305   310   315   320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
            325   330   335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340   345   350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
        355   360   365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370   375   380
Ser Thr Ala Leu Glu Ala Gln Gly Arg Ser Leu Asn Pro Asn Arg Val
385   390   395   400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
            405   410   415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420   425   430

<210> 86
<211> 432
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

<400> 86
His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
1   5   10   15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
            20   25   30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35   40   45

Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
    50   55   60
His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro
65   70   75   80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                85   90   95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100   105   110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115   120   125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130   135   140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145   150   155   160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
                165   170   175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180   185   190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195   200   205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
    210   215   220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225   230   235   240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
            245   250   255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260   265   270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275   280   285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
    290   295   300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305   310   315   320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
                325   330   335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340   345   350
Gly Ile Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe
        355   360   365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370   375   380
Ser Thr Ala Leu Glu Ala His Gly Arg Ser Leu Asn Pro Asn Arg Val
385   390   395   400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
                405   410   415
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420   425   430

<210> 87
<211> 432
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 87
His Gly Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro
 1   5   10   15
Met Asn Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu
            20   25   30
Asp Glu Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val
        35   40   45
Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln
    50   55   60
His Leu Ala Asp Ser Lys Asn Asp Asn Asn Ile Phe Leu Ser Pro
65   70   75   80
Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn
                85   90   95
Asp Thr Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser
            100   105   110
Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys
        115   120   125
Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Lys Leu Val Ser Ala Asn
    130   135   140
Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp
145   150   155   160
Ile Ser Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys
                165   170   175
Glu Asn Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn
            180   ·   185   190
Lys Thr Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn
        195   200   205
Glu Leu Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu
        210   215   220
Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr
225   230   235   240
Lys Ala Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly
            245   250   255
Lys Phe Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu
            260   265   270
Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro
        275   280   285
Glu Lys Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu
        290   295   300
Gln Glu Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met
305   310   315   320
Pro Arg Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln
            325   330   335
Asp Met Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro
            340   ·   345   350
Gly Ile Val Ala Glu Gly Arg Asp Leu Tyr Val Ser Asp Ala Phe
        355   360   365
His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala
    370   375   380
Ser Thr Ala Leu Glu Ala Tyr Gly Arg Ser Leu Asn Pro Asn Arg Val
385   390   395   400
Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro
            405   410   415
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```
Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
            420                 425                 430

<210> 88
<211> 423
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 88
Arg Asp Ile Pro Val Asn Pro Ile Cys Ile Tyr Arg Asn Pro Glu Lys
1               5                   10                  15
Lys Pro Gln Glu Arg Arg Gly Ala Gly Ala Gly Glu Gly Gln Asp Pro
            20                  25                  30
Gly Val His Lys Pro Pro Val Trp Glu Leu Ser Arg Ala Asn Ser Arg
        35                  40                  45
Phe Ala Val Val Phe Tyr Lys His Leu Ala Asp Ser Lys Asp Asn Glu
    50                  55                  60
Glu Asn Ile Phe Leu Ser Pro Leu Ser Ile Ser Thr Ala Phe Ala Met
65                  70                  75                  80
Thr Lys Leu Gly Ala Cys Gly Asp Thr Leu Gln Gln Leu Met Glu Val
            85                  90                  95
Phe Gln Phe Asp Thr Ile Ser Glu Lys Thr Ser Asp Gln Val His Phe
            100                 105                 110
Phe Phe Ala Lys Leu Asn Cys Arg Leu Tyr Lys Lys Ala Asn Lys Ser
        115                 120                 125
Ser Glu Leu Ile Ser Ala Asn Arg Leu Phe Gly Glu Lys Ser Leu Val
    130                 135                 140
Phe Asn Glu Thr Tyr Gln Asn Ile Ser Glu Ile Val Tyr Gly Ala Lys
145                 150                 155                 160
Leu Trp Pro Leu Asn Phe Lys Glu Lys Pro Glu Leu Ser Arg Lys Ile
                165                 170                 175
Ile Asn Glu Trp Val Ala Asn Lys Thr Glu Arg Arg Ile Thr Glu Val
            180                 185                 190
Ile Pro Glu Lys Gly Ile Asp Asp Leu Thr Val Leu Val Leu Val Asn
            195                 200                 205
Thr Ile Tyr Phe Lys Gly His Trp Lys Ser Gln Phe Pro Ala Pro Asn
    210                 215                 220
Thr Arg Leu Asp Leu Phe His Lys Ala Asn Gly Glu Thr Cys Asn Val
225                 230                 235                 240
Pro Ile Met Tyr Gln Glu Ser Arg Phe Pro Tyr Ala Phe Ile Gln Glu
                245                 250                 255
Asp Lys Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr
            260                 265                 270
Met Val Leu Val Leu Pro Lys Ala Gly Thr Pro Leu Val Glu Val Glu
            275                 280                 285
Arg Asp Leu Thr Ser Asp Lys Leu Gln Asp Trp Ile Asp Ser Met Met
    290                 295                 300
Glu Val Ser Leu Thr Val Ser Phe Pro Arg Phe Arg Val Glu Asp Ser
305                 310                 315                 320
Phe Ser Val Lys Glu Lys Leu Arg Lys Met Gly Leu Glu Asp Leu Phe
            325                 330                 335
Ser Pro Glu Asn Ala Lys Leu Pro Gly Ile Val Ala Gly Asp Arg Thr
            340                 345                 350
Asp Leu Tyr Val Ser Glu Ala Phe His Lys Ala Phe Leu Glu Val Asn
        355                 360                 365
Glu Glu Gly Ser Glu Ala Ser Ala Ala Thr Ala Val Val Ile Ser Gly
370                 375                 380
Arg Ser Phe Pro Met Asn Arg Ile Ile Phe Glu Ala Asn Arg Pro Phe
```

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```
385                   390                  395                      400
Leu Leu Phe Ile Arg Glu Ala Thr Leu Asn Thr Ile Ile Phe Met Gly
                405                  410                  415
Arg Ile Ser Asp Pro Cys Ser
            420
```

<210> 89
<211> 456

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 89
```
Met Tyr Leu Leu Ser Leu Leu Leu Leu Ser Leu Leu Gly Ser Ala Tyr
 1               5                  10                  15
Leu Gln Pro Gln His Ala Asp Ile Cys Leu Ala Lys Pro Lys Asp Ile
            20                  25                  30
Pro Leu Thr Pro Met Cys Val Tyr Arg Lys Pro Leu Glu Val Val Glu
            35                  40                  45
Thr Glu Glu Lys Glu Lys Glu Pro Thr Thr Gln Glu Gln Lys Val Pro
            50                  55                  60
Glu Ser Thr Asn Pro Arg Val Tyr Glu Leu Ser Gln Ala Asn Ala Lys
65                  70                  75                  80
Phe Ala Ile Ala Phe Tyr Lys Asn Leu Ala Asp Ser Lys Arg Asp Lys
                85                  90                  95
Glu Asn Ile Phe Met Ser Pro Leu Ser Ile Ser Gln Ala Phe Thr Met
            100                 105                 110
Ala Lys Leu Gly Ala Cys Asn Asn Thr Leu Lys Gln Leu Met Glu Val
            115                 120                 125
Phe His Phe Asp Thr Val Ser Glu Arg Ala Ser Asp Gln Ile His Tyr
    130                 135                 140
Phe Phe Ala Lys Leu Asn Cys Arg Leu Phe Arg Lys Ala Asn Lys Ser
145                 150                 155                 160
Ser Glu Leu Val Ser Val Asn Arg Leu Phe Gly Glu Lys Ser Leu Thr
                165                 170                 175
Phe Asn Glu Thr Tyr Gln Asp Ile Ser Glu Ile Val Tyr Gly Ala Lys
            180                 185                 190
Leu Trp Pro Leu Asn Phe Arg Asp Lys Pro Glu Leu Ser Arg Glu Ile
            195                 200                 205
Ile Asn Asn Trp Val Ser Asn Lys Thr Glu Lys Arg Ile Thr Asp Val
    210                 215                 220
Ile Pro Lys Asp Ala Ile Thr Pro Asp Thr Val Leu Val Leu Ile Asn
225                 230                 235                 240
Ala Ile Tyr Phe Lys Gly Leu Trp Lys Ser Lys Phe Asn Ser Glu Asn
                245                 250                 255
Thr Lys Met Asp Gln Phe His Pro Ala Lys Asn Ser Asn Cys Leu Thr
            260                 265                 270
Ala Thr Met Tyr Gln Glu Gly Thr Phe Arg Tyr Gly Ser Phe Lys Asp
            275                 280                 285
Asp Gly Val Gln Val Leu Glu Leu Pro Tyr Lys Gly Asp Asp Ile Thr
    290                 295                 300
Met Val Leu Val Leu Pro Ser Gln Glu Thr Pro Leu Thr Thr Val Glu
305                 310                 315                 320
Gln Asn Leu Thr Leu Glu Lys Leu Gly Asn Trp Leu Gln Lys Ser Arg
                325                 330                 335
Glu Leu Gln Leu Ser Val Tyr Leu Pro Arg Phe Arg Val Glu Asp Ser
            340                 345                 350
Phe Ser Val Lys Glu Lys Leu Gln Glu Met Gly Leu Val Asp Leu Phe
    355                 360                 365
```

```
Asp Pro Asn Ser Ala Lys Leu Pro Gly Ile Ile Ala Gly Gly Arg Thr
    370             375             380
Asp Leu Tyr Val Ser Asp Ala Phe His Lys Ala Phe Leu Glu Val Asn
385             390             395             400
Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr Ala Val Ile Leu Thr Gly
            405             410             415

Arg Ser Leu Asn Leu Asn Arg Ile Ile Phe Arg Ala Asn Arg Pro Phe
            420             425             430
Leu Val Phe Ile Arg Glu Val Ala Ile Asn Ala Ile Leu Phe Met Gly
        435             440             445
Arg Val Ala Asn Pro Cys Thr Glu
    450             455
```

<210> 90
<211> 465
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 90
```
Met Tyr Ser Pro Gly Ala Gly Ser Gly Ala Ala Gly Glu Arg Lys Leu
1               5               10              15
Cys Leu Leu Ser Leu Leu Leu Ile Gly Ala Leu Gly Cys Ala Ile Cys
            20              25              30
His Gly Asn Pro Val Asp Asp Ile Cys Ile Ala Lys Pro Arg Asp Ile
        35              40              45
Pro Val Asn Pro Leu Cys Ile Tyr Arg Ser Pro Gly Lys Lys Ala Thr
    50              55              60
Glu Glu Asp Gly Ser Glu Gln Lys Val Pro Glu Ala Thr Asn Arg Arg
65              70              75              80
Val Trp Glu Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Asn Phe Tyr
            85              90              95
Gln His Leu Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser
            100             105             110
Pro Leu Ser Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys
        115             120             125
Asn Asp Thr Leu Lys Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile
    130             135             140
Ser Glu Lys Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn
145             150             155             160
Cys Arg Leu Tyr Arg Lys Ala Asn Lys Ser Ser Asp Leu Val Ser Ala
            165             170             175
Asn Arg Leu Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Ser Tyr Gln
            180             185             190
Asp Val Ser Glu Val Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe
            195             200             205
Lys Glu Asn Pro Glu Gln Ser Arg Val Thr Ile Asn Asn Trp Val Ala
    210             215             220
Asn Lys Thr Glu Gly Arg Ile Lys Asp Val Ile Pro Gln Gly Ala Ile
225             230             235             240
Asn Glu Leu Thr Ala Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly
            245             250             255
Leu Trp Lys Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Pro Phe
            260             265             270
Tyr Lys Val Asp Gly Gln Ser Cys Pro Val Pro Met Met Tyr Gln Glu
    275             280             285
Gly Lys Phe Lys Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu
    290             295             300
Leu Pro Phe Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys
```

```
305                 310                 315                 320
Pro Glu Lys Ser Leu Ala Lys Val Glu Gln Glu Leu Thr Pro Glu Leu
                325                 330                 335
Leu Gln Glu Trp Leu Asp Glu Leu Ser Glu Thr Met Leu Val Val His
                340                 345                 350
Met Pro Arg Phe Arg Thr Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu
        355                 360                 365
Gln Asp Met Gly Leu Ile Asp Leu Phe Ser Pro Glu Lys Ser Gln Leu
    370                 375                 380
Pro Gly Ile Val Ala Gly Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala
385                 390                 395                 400
Phe His Lys Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala
                405                 410                 415
Ala Ser Thr Ser Val Val Ile Thr Gly Arg Ser Leu Asn Pro Asn Arg
                420                 425                 430
Val Thr Phe Lys Ala Asn Arg Pro Phe Leu Val Leu Ile Arg Glu Val
                435                 440                 445
Ala Leu Asn Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val
    450                 455     .           460
Asn
465
```

<210> 91
<211> 1599
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
        synthetic construct

<400> 91
```
caccagcatc atctcctcca attcatccag ctactctgcc catgaagata atagttttca    60
ggcggattgc ctcagatcac actatctcca cttgcccagc cctgtggaag attagcggcc   120
atgtattcca atgtgatagg aactgtaacc tctggaaaaa ggaaggttta tctttttgtcc  180
ttgctgctca ttggcttctg ggactgcgtg acctgtcacg ggagccctgt ggacatctgc   240
acagccaagc cgcgggacat tcccatgaat cccatgtgca tttaccgctc cccggagaag   300
aaggcaactg aggatgaggg ctcagaacag aagatcccgg aggccaccaa ccggcgtgtc   360
tgggaactgt ccaaggccaa ttcccgcttt gctaccactt tctatcagca cctggcagat   420
tccaagaatg acaatgataa catttttcctg tcacccctga gtatctccac ggcttttgct   480
atgaccaagc tgggtgcctg taatgacacc ctccagcaac tgatggaggt atttaagttt   540
gacaccatat ctgagaaaac atctgatcag atccacttct tctttgccaa actgaactgc   600
cgactctatc gaaaagccaa caaatcctcc aagttagtat cagccaatcg ccttttttgga   660
gacaaatccc ttaccttcaa tgagacctac caggacatca gtgagttggt atatggagcc   720
aagctccagc ccctggactt caaggaaaat gcagagcaat ccagagcggc catcaacaaa   780
tgggtgtcca ataagaccga aggccgaatc accgatgtca ttccctcgga agccatcaat   840
gagctcactg ttctggtgct ggttaacacc atttacttca agggcctgtg gaagtcaaag   900
ttcagccctg agaacacaag gaaggaactg ttctacaagg ctgatggaga gtcgtgttca   960
gcatctatga tgtaccagga aggcaagttc cgttatcggc gcgtggctga aggcacccag  1020
gtgcttgagt tgcccttcaa aggtgatgac atcaccatgg tcctcatctt gcccaagcct  1080
gagaagagcc tggccaaggt ggagaaggaa ctcaccccag aggtgctgca ggagtggctg  1140
gatgaattgg aggagatgat gctggtggtt cacatgcccc gcttccgcat tgaggacggc  1200
ttcagtttga aggagcagct gcaagacatg ggccttgtcg atctgttcag ccctgaaaag  1260
tccaaactcc caggtattgt tgcagaaggc cgagatgacc tctatgtctc agatgcattc  1320
cataaggcat ttcttgaggt aaatgaagaa ggcagtgaag cagctgcaag taccgctgtt  1380
gtgattgctg gccgttcgct aaacccccaac agggtgactt tcaaggcaa caggcccttc   1440
ctggttttta taagagaagt tcctctgaac actattatct tcatgggcag agtagccaac  1500
ccttgtgtta agtaaaatgt tcttattctt tgcacctctt cctattttg gtttgtgaac   1560
agaagtaaaa ataaatacaa actacttcca tctcacatt                          1599
```

<210> 92
<211> 430
<212> PRT

<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
       synthetic construct

<221> VARIANT
<222> (386)...(389)
<223> Xaa = any amino acid

<400> 92
```
Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1               5                   10              15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
            20                  25              30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35                  40              45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
    50                  55              60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65                  70                  75                  80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
                85                  90                  95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100                 105                 110
Thr Ser Asp Gln Ile His Phe Phe Ala Lys Leu Asn Cys Arg Leu
        115                 120                 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
    130                 135                 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                 150                 155                 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
            165                 170                 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180                 185                 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
        195                 200                 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
    210                 215                 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                 230                 235                 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                 250                 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260                 265                 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
        275                 280                 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
    290                 295                 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                 310                 315                 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                 330                 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340                 345                 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355                 360                 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
    370                 375                 380
Ala Xaa Xaa Xaa Xaa Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
385                 390                 395                 400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
            405                 410                 415
```

```
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
        420                 425                 430
```

<210> 93
<211> 430
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:/note =
      synthetic construct

<400> 93
```
Ser Pro Val Asp Ile Cys Thr Ala Lys Pro Arg Asp Ile Pro Met Asn
1               5                   10                  15
Pro Met Cys Ile Tyr Arg Ser Pro Glu Lys Lys Ala Thr Glu Asp Glu
        20                  25                  30
Gly Ser Glu Gln Lys Ile Pro Glu Ala Thr Asn Arg Arg Val Trp Glu
        35                  40                  45
Leu Ser Lys Ala Asn Ser Arg Phe Ala Thr Thr Phe Tyr Gln His Leu
        50                  55                  60
Ala Asp Ser Lys Asn Asp Asn Asp Asn Ile Phe Leu Ser Pro Leu Ser
65                  70                  75                  80
Ile Ser Thr Ala Phe Ala Met Thr Lys Leu Gly Ala Cys Asn Asp Thr
                85                  90                  95
Leu Gln Gln Leu Met Glu Val Phe Lys Phe Asp Thr Ile Ser Glu Lys
            100                 105                 110
Thr Ser Asp Gln Ile His Phe Phe Phe Ala Lys Leu Asn Cys Arg Leu
            115                 120                 125
Tyr Arg Lys Ala Asn Lys Ala Ser Lys Leu Val Ser Ala Asn Arg Leu
        130                 135                 140
Phe Gly Asp Lys Ser Leu Thr Phe Asn Glu Thr Tyr Gln Asp Ile Ser
145                 150                 155                 160
Glu Leu Val Tyr Gly Ala Lys Leu Gln Pro Leu Asp Phe Lys Glu Asn
                165                 170                 175
Ala Glu Gln Ser Arg Ala Ala Ile Asn Lys Trp Val Ser Asn Lys Thr
            180                 185                 190
Glu Gly Arg Ile Thr Asp Val Ile Pro Ser Glu Ala Ile Asn Glu Leu
            195                 200                 205
Thr Val Leu Val Leu Val Asn Thr Ile Tyr Phe Lys Gly Leu Trp Lys
            210                 215                 220
Ser Lys Phe Ser Pro Glu Asn Thr Arg Lys Glu Leu Phe Tyr Lys Ala
225                 230                 235                 240
Asp Gly Glu Ser Cys Ser Ala Ser Met Met Tyr Gln Glu Gly Lys Phe
                245                 250                 255
Arg Tyr Arg Arg Val Ala Glu Gly Thr Gln Val Leu Glu Leu Pro Phe
            260                 265                 270
Lys Gly Asp Asp Ile Thr Met Val Leu Ile Leu Pro Lys Pro Glu Lys
            275                 280                 285
Ser Leu Ala Lys Val Glu Lys Glu Leu Thr Pro Glu Val Leu Gln Glu
        290                 295                 300
Trp Leu Asp Glu Leu Glu Glu Met Met Leu Val Val His Met Pro Arg
305                 310                 315                 320
Phe Arg Ile Glu Asp Gly Phe Ser Leu Lys Glu Gln Leu Gln Asp Met
                325                 330                 335
Gly Leu Val Asp Leu Phe Ser Pro Glu Lys Ser Lys Leu Pro Gly Ile
            340                 345                 350
Val Ala Glu Gly Arg Asp Asp Leu Tyr Val Ser Asp Ala Phe His Lys
        355                 360                 365
Ala Phe Leu Glu Val Asn Glu Glu Gly Ser Glu Ala Ala Ala Ser Thr
        370                 375                 380
Ala Val Val Ile Ala Gly Arg Ser Leu Asn Pro Asn Arg Val Thr Phe
```
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```
385                     390                 395                     400
Lys Ala Asn Arg Pro Phe Leu Val Phe Ile Arg Glu Val Pro Leu Asn
                    405                 410                 415
Thr Ile Ile Phe Met Gly Arg Val Ala Asn Pro Cys Val Lys
                420                 425                 430
```